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* * * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1           Web Page for STN Seminar Schedule - N. America
 NEWS  2  JAN 02   STN pricing information for 2008 now available
 NEWS  3  JAN 16   CAS patent coverage enhanced to include exemplified
                   prophetic substances
 NEWS  4  JAN 28   USPATFULL, USPAT2, and USPATOLD enhanced with new
                   custom IPC display formats
 NEWS  5  JAN 28   MARPAT searching enhanced
 NEWS  6  JAN 28   USGENE now provides USPTO sequence data within 3 days
                   of publication
 NEWS  7  JAN 28   TOXCENTER enhanced with reloaded MEDLINE segment
 NEWS  8  JAN 28   MEDLINE and LMEDLINE reloaded with enhancements
 NEWS  9  FEB 08   STN Express, Version 8.3, now available
 NEWS 10  FEB 20   PCI now available as a replacement to DPCI
 NEWS 11  FEB 25   IFIREF reloaded with enhancements
 NEWS 12  FEB 25   IMSPRODUCT reloaded with enhancements
 NEWS 13  FEB 29   WPINDEX/WPIDS/WPIX enhanced with ECLA and current
                   U.S. National Patent Classification
 NEWS 14  MAR 31   IFICDB, IFIPAT, and IFIUDB enhanced with new custom
                   IPC display formats
 NEWS 15  MAR 31   CAS REGISTRY enhanced with additional experimental
                   spectra
 NEWS 16  MAR 31   CA/CAplus and CASREACT patent number format for U.S.
                   applications updated
 NEWS 17  MAR 31   LPCI now available as a replacement to LDPCI
 NEWS 18  MAR 31   EMBASE, EMBAL, and LEMBASE reloaded with enhancements
 NEWS 19  APR 04   STN AnaVist, Version 1, to be discontinued
 NEWS 20  APR 15   WPIDS, WPINDEX, and WPIX enhanced with new
                   predefined hit display formats
 NEWS 21  APR 28   EMBASE Controlled Term thesaurus enhanced
 NEWS 22  APR 28   IMSRESEARCH reloaded with enhancements
 NEWS 23  MAY 30   INPAFAMDB now available on STN for patent family
                   searching
 NEWS 24  MAY 30   DGENE, PCTGEN, and USGENE enhanced with new homology
                   sequence search option
 NEWS 25  JUN 06   EPFULL enhanced with 260,000 English abstracts
 NEWS 26  JUN 06   KOREAPAT updated with 41,000 documents

 NEWS EXPRESS FEBRUARY 08 CURRENT WINDOWS VERSION IS V8.3,
              AND CURRENT DISCOVER FILE IS DATED 20 FEBRUARY 2008

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FILE 'HOME' ENTERED AT 09:39:40 ON 11 JUN 2008

=> index bioscience
FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.21       0.21

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
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      AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
      CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
      DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 09:40:08 ON 11 JUN 2008

69 FILES IN THE FILE LIST IN STNINDEX

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search error messages that display as 0* with SET DETAIL OFF.

=> s information and architecture and object and name and (biologic? or taxonomic? or gene or
  12 FILES SEARCHED...
  21 FILES SEARCHED...
  30 FILES SEARCHED...
        4   FILE IFIPAT
  47 FILES SEARCHED...
        1   FILE PHIN
        9   FILE PROMT
  60 FILES SEARCHED...
     1479   FILE USPATFULL
      331   FILE USPAT2
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L1   QUE INFORMATION AND ARCHITECTURE AND OBJECT AND NAME AND (BIOLOGIC? OR TAX
       ONOMIC? OR GENE OR PROTEIN) AND RESOURCE AND IDENTIFIER

=> file medline caplus scisearch embase
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     3.90       4.11

FILE 'MEDLINE' ENTERED AT 09:43:33 ON 11 JUN 2008

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=> s information and object and (biologic? or taxonomic? or gene or protein) and resource and
L2          19 INFORMATION AND OBJECT AND (BIOLOGIC? OR TAXONOMIC? OR GENE OR
               PROTEIN) AND RESOURCE AND IDENTIFIER

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PROCESSING COMPLETED FOR L2
L3           10 DUP REM L2 (9 DUPLICATES REMOVED)

=> d bib ab 1-10

L3   ANSWER 1 OF 10     MEDLINE on STN
Full Text
AN   2008357957     IN-PROCESS
DN   PubMed ID: 18495032
TI   A plant resource and experiment management system based on the Golm
     Plant Database as a basic tool for omics research.
AU   Kohl Karin I; Basler Georg; Ludemann Alexander; Selbig Joachim; Walther
     Dirk
CS   Max-Planck-Institute of Molecular Plant Physiology, Am Muhlenberg 1, 14476
     Golm, Germany.. koehl@mpimp-golm.mpg.de
SO   Plant methods, (2008) Vol. 4, pp. 11.  Electronic Publication: 2008-05-21.
     Journal code: 101245798. E-ISSN: 1746-4811.
CY   England: United Kingdom
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   NONMEDLINE; IN-DATA-REVIEW; IN-PROCESS; NONINDEXED
ED   Entered STN: 5 Jun 2008
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Last Updated on STN: 5 Jun 2008

AB ABSTRACT: BACKGROUND: For omics experiments, detailed characterisation of experimental material with respect to its genetic features, its cultivation history and its treatment history is a requirement for analyses by bioinformatics tools and for publication needs. Furthermore, meta-analysis of several experiments in systems biology based approaches make it necessary to store this **information** in a standardised manner, preferentially in relational databases. In the Golm Plant Database System, we devised a data management system based on a classical Laboratory **Information** Management System combined with web-based user interfaces for data entry and retrieval to collect this **information** in an academic environment. RESULTS: The database system contains modules representing the genetic features of the germplasm, the experimental conditions and the sampling details. In the germplasm module, genetically identical lines of **biological** material are generated by defined workflows, starting with the import workflow, followed by further workflows like genetic modification (transformation), vegetative or sexual reproduction. The latter workflows link lines and thus create pedigrees. For experiments, plant **objects** are generated from plant lines and united in so-called cultures, to which the cultivation conditions are linked. Materials and methods for each cultivation step are stored in a separate ACCESS database of the plant cultivation unit. For all cultures and thus every plant **object**, each cultivation site and the culture's arrival time at a site are logged by a barcode-scanner based system. Thus, for each plant **object**, all site-related parameters, e.g. automatically logged climate data, are available. These life history data and genetic **information** for the plant **objects** are linked to analytical results by the sampling module, which links sample components to plant **object identifiers**. This workflow uses controlled vocabulary for organs and treatments. Unique names generated by the system and barcode labels facilitate identification and management of the material. Web pages are provided as user interfaces to facilitate maintaining the system in an environment with many desktop computers and a rapidly changing user community. Web based search tools are the basis for joint use of the material by all researchers of the institute. CONCLUSION: The Golm Plant Database system, which is based on a relational database, collects the genetic and environmental **information** on plant material during its production or experimental use at the Max-Planck-Institute of Molecular Plant Physiology. It thus provides **information** according to the MIAME standard for the component 'Sample' in a highly standardised format. The Plant Database system thus facilitates collaborative work and allows efficient queries in data analysis for systems biology research.

L3 ANSWER 2 OF 10 MEDLINE on STN DUPLICATE 1
Full Text
AN 2005528226 MEDLINE
DN PubMed ID: 16204117
TI Web servicing the **biological** office.
AU Szugat Martin; Guttler Daniel; Fundel Katrin; Sohler Florian; Zimmer Ralf
CS Department of Informatics, Ludwig-Maximilians-Universitat Munchen, Munchen, Germany.. prothesaurus@bio.ifi.lmu.de
SO Bioinformatics (Oxford, England), (2005 Sep 1) Vol. 21 Suppl 2, pp. ii268-9.
Journal code: 9808944. E-ISSN: 1460-2059.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200708
ED Entered STN: 6 Oct 2005
Last Updated on STN: 15 Dec 2005
Entered Medline: 27 Aug 2007
AB Biologists routinely use Microsoft Office applications for standard analysis tasks. Despite ubiquitous internet **resources**, **information** needed for everyday work is often not directly and seamlessly available. Here we describe a very simple and easily extendable mechanism using Web Services to enrich standard MS Office applications with internet **resources**. We demonstrate its capabilities by providing a Web-based thesaurus for **biological objects**, which maps names to database **identifiers** and vice versa via an appropriate synonym list. The client application ProTag makes these features available in MS Office

applications using Smart Tags and Add-Ins. AVAILABILITY: http://services.bio.ifi.lmu.de/prothesaurus/

L3 ANSWER 3 OF 10 MEDLINE on STN DUPLICATE 2
Full Text
AN 2005128842 MEDLINE
DN PubMed ID: 15759623
TI Linking ontological **resources** using aggregatable substance **identifiers** to organize extracted relations.
AU Marshall Byron; Su Hua; McDonald Daniel; Chen Hsinchun
CS MIS Department, University of Arizona, Tucson, Arizona 85721, USA.. byronm@eller.arizona.edu
NC 1 R33 LM07299-01 (United States NLM)
SO Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing, (2005) pp. 162-73.
Journal code: 9711271. ISSN: 1793-5091.
CY Singapore
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LA English
FS Priority Journals
EM 200504
ED Entered STN: 12 Mar 2005
Last Updated on STN: 12 Apr 2005
Entered Medline: 11 Apr 2005
AB Systems that extract **biological** regulatory pathway relations from free-text sources are intended to help researchers leverage vast and growing collections of research literature. Several systems to extract such relations have been developed but little work has focused on how those relations can be usefully organized (aggregated) to support visualization systems or analysis algorithms. Ontological **resources** that enumerate name strings for different types of biomedical **objects** should play a key role in the organization process. In this paper we delineate five potentially useful levels of relational granularity and propose the use of aggregatable substance **identifiers** to help reduce lexical ambiguity. An aggregatable substance **identifier** applies to a **gene** and its products. We merged 4 extensive lexicons and compared the extracted strings to the text of five million MEDLINE abstracts. We report on the ambiguity within and between name strings and common English words. Our results show an 89% reduction in ambiguity for the extracted human substance name strings when using an aggregatable substance approach.

L3 ANSWER 4 OF 10 MEDLINE on STN DUPLICATE 3
Full Text
AN 2004641263 MEDLINE
DN PubMed ID: 15608167
TI The Universal **Protein Resource** (UniProt).
AU Bairoch Amos; Apweiler Rolf; Wu Cathy H; Barker Winona C; Boeckmann Brigitte; Ferro Serenella; Gasteiger Elisabeth; Huang Hongzhan; Lopez Rodrigo; Magrane Michele; Martin Maria J; Natale Darren A; O'Donovan Claire; Redaschi Nicole; Yeh Lai-Su L
CS Swiss Institute of Bioinformatics, Centre Medical Universitaire, 1 rue Michel Servet, 1211 Geneva 4, Switzerland.
NC 1R01HG02273-01 (United States NHGRI)
U01 HG02712-01 (United States NHGRI)
SO Nucleic acids research, (2005 Jan 1) Vol. 33, No. Database issue, pp. D154-9.
Journal code: 0411011. E-ISSN: 1362-4962.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
(RESEARCH SUPPORT, U.S. GOV'T, P.H.S.)
LA English
FS Priority Journals
EM 200504
ED Entered STN: 28 Dec 2004
Last Updated on STN: 17 Apr 2005
Entered Medline: 15 Apr 2005
AB The Universal **Protein Resource** (UniProt) provides the scientific community with a single, centralized, authoritative **resource** for

protein sequences and functional **information**. Formed by uniting the Swiss-Prot, TrEMBL and PIR **protein** database activities, the UniProt consortium produces three layers of **protein** sequence databases: the UniProt Archive (UniParc), the UniProt Knowledgebase (UniProt) and the UniProt Reference (UniRef) databases. The UniProt Knowledgebase is a comprehensive, fully classified, richly and accurately annotated **protein** sequence knowledgebase with extensive cross-references. This centrepiece consists of two sections: UniProt/Swiss-Prot, with fully, manually curated entries; and UniProt/TrEMBL, enriched with automated classification and annotation. During 2004, tens of thousands of Knowledgebase records got manually annotated or updated; we introduced a new comment line topic: TOXIC DOSE to store **information** on the acute toxicity of a toxin; the UniProt keyword list got augmented by additional keywords; we improved the documentation of the keywords and are continuously overhauling and standardizing the annotation of post-translational modifications. Furthermore, we introduced a new documentation file of the strains and their synonyms. Many new database cross-references were introduced and we started to make use of Digital **Object Identifiers**. We also achieved in collaboration with the Macromolecular Structure Database group at EBI an improved integration with structural databases by residue level mapping of sequences from the **Protein** Data Bank entries onto corresponding UniProt entries. For convenient sequence searches we provide the UniRef non-redundant sequence databases. The comprehensive UniParc database stores the complete body of publicly available **protein** sequence data. The UniProt databases can be accessed online (http://www.uniprot.org) or downloaded in several formats (ftp://ftp.uniprot.org/pub). New releases are published every two weeks.

L3 ANSWER 5 OF 10 EMBASE COPYRIGHT (c) 2008 Elsevier B.V. All rights
Full Text
reserved on STN DUPLICATE 4
AN 2006141216 EMBASE
TI The Universal **Protein Resource** (UniProt).
AU Bairoch, Amos; Boeckmann, Brigitte; Ferro, Serenella; Gasteiger, Elisabeth; Redaschi, Nicole
CS Swiss Institute of Bioinformatics, Centre Medical Universitaire, 1 rue Michel Servet, 1211 Geneva 4, Switzerland.
AU Apweiler, Rolf (correspondence); Lopez, Rodrigo; Magrane, Michele; Martin, Maria J.; O'Donovan, Claire
CS The EMBL Outstation, The European Bioinformatics Institute, Hinxton, Cambridge CB10 1SD, United Kingdom. apweiler@ebi.ac.uk
AU Wu, Cathy H.; Huang, Hongzhan; Natale, Darren A.
CS Department of Biochemistry and Molecular Biology, Georgetown University Medical Center, 3900 Reservoir Road NW, Washington, DC 20057-1414, United States.
AU Barker, Winona C.; Yeh, Lai-Su L.
CS National Biomedical Research Foundation, Georgetown University Medical Center, 3900 Reservoir Road NW, Washington, DC 20057-1414, United States.
SO Nucleic Acids Research, (Jan 2005) Vol. 33, No. SUPPL. 1, pp. D154-D159. Refs: 30
ISSN: 0305-1048 E-ISSN: 1362-4962 CODEN: NARHAD
CY United Kingdom
DT Journal; Article
FS 027 Biophysics, Bioengineering and Medical Instrumentation
029 Clinical and Experimental Biochemistry
052 Toxicology
LA English
SL English
ED Entered STN: 10 Apr 2006
Last Updated on STN: 10 Apr 2006
AB The Universal **Protein Resource** (UniProt) provides the scientific community with a single, centralized, authoritative **resource** for **protein** sequences and functional **information**. Formed by uniting the Swiss-Prot, TrEMBL and PIR **protein** database activities, the UniProt consortium produces three layers of **protein** sequence databases: the UniProt Archive (UniParc), the UniProt Knowledgebase (UniProt) and the UniProt Reference (UniRef) databases. The UniProt Knowledgebase is a comprehensive, fully classified, richly and accurately annotated **protein** sequence knowledgebase with extensive cross-references. This centrepiece consists of two sections: UniProt/Swiss-Prot, with fully, manually curated entries; and UniProt/TrEMBL, enriched with automated classification and annotation. During 2004, tens of thousands of Knowledgebase records got

manually annotated or updated; we introduced a new comment line topic: TOXIC DOSE to store **information** on the acute toxicity of a toxin; the UniProt keyword list got augmented by additional keywords; we improved the documentation of the keywords and are continuously overhauling and standardizing the annotation of post-translational modifications. Furthermore, we introduced a new documentation file of the strains and their synonyms. Many new database cross-references were introduced and we started to make use of Digital **Object Identifiers**. We also achieved in collaboration with the Macromolecular Structure Database group at EBI an improved integration with structural databases by residue level mapping of sequences from the **Protein** Data Bank entries onto corresponding UniProt entries. For convenient sequence searches we provide the UniRef non-redundant sequence databases. The comprehensive UniParc database stores the complete body of publicly available **protein** sequence data. The UniProt databases can be accessed online (http://www.uniprot.org) or downloaded in several formats (ftp://ftp.uniprot.org/pub). New releases are published every two weeks. © 2005 Oxford University Press.

L3 ANSWER 6 OF 10 EMBASE COPYRIGHT (c) 2008 Elsevier B.V. All rights Full Text
reserved on STN
AN 2005487550 EMBASE
TI Web servicing the **biological** office.
AU Szugat, Martin (correspondence); Guttler, Daniel; Fundel, Katrin; Sohler, Florian; Zimmer, Ralf
CS Department of Informatics, Ludwig-Maximilians-Universitat Munchen, 80333 Munchen, Germany. prothesaurus@bio.ifi.lmu.de
SO Bioinformatics, (Sep 2005) Vol. 21, No. SUPPL. 2, pp. ii268-ii269. Refs: 7
ISSN: 1367-4803 E-ISSN: 1460-2059 CODEN: BOINFP
CY United Kingdom
DT Journal; Article
FS 027 Biophysics, Bioengineering and Medical Instrumentation
029 Clinical and Experimental Biochemistry
LA English
SL English
ED Entered STN: 17 Nov 2005
Last Updated on STN: 17 Nov 2005
AB Summary: Biologists routinely use Microsoft Office applications for standard analysis tasks. Despite ubiquitous internet **resources**, **information** needed for everyday work is often not directly and seamlessly available. Here we describe a very simple and easily extendable mechanism using Web Services to enrich standard MS Office applications with internet **resources**. We demonstrate its capabilities by providing a Web-based thesaurus for **biological objects**, which maps names to database **identifiers** and vice versa via an appropriate synonym list. The client application ProTag makes these features available in MS Office applications using Smart Tags and Add-Ins. © The Author 2005. Published by Oxford University Press. All rights reserved.

L3 ANSWER 7 OF 10 MEDLINE on STN DUPLICATE 5
Full Text
AN 2003538319 MEDLINE
DN PubMed ID: 14618567
TI GIMS: an integrated data storage and analysis environment for genomic and functional data.
AU Cornell Michael; Paton Norman W; Hedeler Cornelia; Kirby Paul; Delneri Daniela; Hayes Andrew; Oliver Stephen G
CS Department of Computer Science, University of Manchester, Manchester M13 9PL, UK.
SO Yeast (Chichester, England), (2003 Nov) Vol. 20, No. 15, pp. 1291-306. Journal code: 8607637. ISSN: 0749-503X.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
LA English
FS Priority Journals
EM 200402
ED Entered STN: 18 Nov 2003
Last Updated on STN: 4 Feb 2004
Entered Medline: 3 Feb 2004
AB Effective analyses in functional genomics require access to many kinds of

biological data. For example, the analysis of upregulated **genes** in a microarray experiment might be aided by **information** concerning **protein** interactions or **proteins'** cellular locations. However, such **information** is often stored in different formats at different sites, in ways that may not be amenable to integrated analysis. The Genome **Information** Management System (GIMS) is an **object** database that integrates genomic data with data on the transcriptome, **protein-protein** interactions, metabolic pathways and annotations, such as **gene** ontology terms and **identifiers**. The resulting system supports the running of analyses over this integrated data **resource**, and provides comprehensive facilities for handling and interrelating the results of these analyses. GIMS has been used to store Saccharomyces cerevisiae data, and we demonstrate how the integrated storage of diverse types of data can be beneficial for analysis, using combinations of complex queries. As an example, we describe how GIMS has been used to analyse a collection of aryl alcohol dehydrogenase **gene** deletion mutants. The GIMS database can be accessed remotely using a Java application that can be downloaded from http://img.cs.man.ac.uk/gims.

L3 ANSWER 8 OF 10 SCISEARCH COPYRIGHT (c) 2008 The Thomson
Full Text
Corporation on STN
AN 2003:478917 SCISEARCH
GA The Genuine Article (R) Number: 683LM
TI Integr8: Enhanced inter-operability of European molecular biology databases
AU Kersey P J (Reprint); Morris L; Hermjakob H; Apweiler R
CS European Bioinformat Inst, EMBL Outstation, Wellcome Trust Genome Campus, Cambridge CB10 1SD, England (Reprint); European Bioinformat Inst, EMBL Outstation, Cambridge CB10 1SD, England
CYA England
SO METHODS OF INFORMATION IN MEDICINE, (2003) Vol. 42, No. 2, pp. 154-160. ISSN: 0026-1270.
PB SCHATTAUER GMBH-VERLAG MEDIZIN NATURWISSENSCHAFTEN, HOLDERLINSTRASSE 3, D-70174 STUTTGART, GERMANY.
DT Article; Journal
LA English
REC Reference Count: 12
ED Entered STN: 20 Jun 2003
Last Updated on STN: 20 Jun 2003
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Objectives: The increasing production of molecular biology data in the post-genomic era, and the proliferation of databases that store it, require the development of an integrative layer in database services to facilitate the synthesis of related **information**. The solution of this problem is made more difficult by the absence of universal **identifiers** for **biological** entities, and the breadth and variety of available data.
Methods: Integr8 was modelled using UML (Universal Modelling Language). Integr8 is being implemented as an n-tier system using a modern **object**-oriented programming language (Java). An **object**-relational mapping tool, OJB, is being used to specify the interface between the upper layers and an underlying relational database.
Results. The European Bioinformatics Institute is launching the Integr8 project. Integr8 will be an automatically populated database in which we will maintain stable **identifiers** for **biological** entities, describe their relationships with each other (in accordance with the central dogma of biology), and store equivalences between identified entities in the source databases. Only core data will be stored in Integr8, with web links to the source databases providing further **information**.
Conclusions. Integr8 will provide the integrative layer of the next generation of bioinformatics services from the EBI. Web-based interfaces will be developed to offer **gene**-centric views of the integrated data, presenting (where known) the links between genome, proteome and phenotype.

L3 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN
Full Text
AN 2003:456547 CAPLUS
DN 140:37460
TI Future-proofing **biological** nomenclature
AU Garrity, George M.; Lyons, Catherine

CS Department of Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI, USA
SO OMICS (2003), 7(1), 31-33
CODEN: OMICAE; ISSN: 1536-2310
PB Mary Ann Liebert, Inc.
DT Journal; General Review
LA English
AB A review on several issues and advances in the nomenclature and **taxonomic** classification of **biol.** entities, with particular emphasis on the Digital **Object Identifier** (DOI). A DOI is a unique, persistent **identifier** of an **information resource** that is registered together with a URL. Its purpose is the management and retrieval of that **resource** in the networked environment.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN
Full Text
AN 2002:622377 CAPLUS
DN 138:67774
TI KEGG for computational genomics
AU Kanehisa, Minoru; Goto, Susumu
CS Institute for Chemical Research, Kyoto University, Kyoto, Japan
SO Current Topics in Computational Molecular Biology (2002), 301-315.
Editor(s): Jiang, Tao; Xu, Ying; Zhang, Michael Q. Publisher: MIT Press, Cambridge, Mass.
CODEN: 69CZGQ; ISBN: 0-262-10092-4
DT Conference
LA English
AB KEGG , the Kyoto Encyclopedia of **Genes** and Genomes (Kanehisa 1997a), is implemented in the PATHWAY, **GENES**, GENOME, Expression, LIGAND, and BRITE (Biomol. Relations in **Information** Transmission and Expression) databases which are all available at the GenomeNet (http://www.genome.adip/). In our view, the genome is simply an **information** storage of how to make individual mol. building blocks of life. The genome does not contain much **information** about the wiring of building blocks - for example, how they interact to make up a cell or to exert cellular functions. The wiring **information** is likely to be distributed in the cell and more dynamic in nature. One of the major objectives of KEGG is to computerize data and knowledge on mol. pathways and complexes that are involved in various cellular processes. Thus, KEGG contains a unique data **object** termed the generalized **protein-protein** interaction network, or simply the network, which is an abstr. network of **gene** products (Kanehisa 2000a, b). KEGG is a computational **resource** for analyzing networks. The network prediction in KEGG is to compute the generalized **protein-protein** interaction network, or the network of **gene** products, from the catalog of **genes** in the genome. The prediction is based on the ref. knowledge of real networks in the PATHWAY database and addnl. **information** of transcriptomes and proteomes in the EXPRESSION and BRITE databases. The problem can be viewed as a conversion of the genome graph to the network graph by integrating addnl. graphs of transcriptomes, proteomes, and similar networks. When an organism-specific pathway is reconstructed by matching **genes** in the genome against KEGG ref. pathways, a few **genes** are often missing in an otherwise complete pathway. Most of the cases can be solved by reexamg. **gene** annotations and assignments of ortholog **identifiers**. KEGG is not suitable for simulating continuous behaviors of the cell because it does not contain any kinetic parameters. However, we still hope that KEGG will become useful to simulate perturbations to the cell, such as **gene** mutations and environmental changes, and their dynamic consequences.
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> file medline

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	44.10	48.21
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-1.60	-1.60

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FILE 'MEDLINE' ENTERED AT 09:45:00 ON 11 JUN 2008

 FILE LAST UPDATED: 10 Jun 2008 (20080610/UP).  FILE COVERS 1949 TO DATE.

  MEDLINE has been updated with the National Library of Medicine's
  revised 2008 MeSH terms.  See HELP RLOAD for details.

  This file contains CAS Registry Numbers for easy and accurate
  substance identification.

  See HELP RANGE before carrying out any RANGE search.

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E1            2     GARRITY F/AU
E2            7     GARRITY F L/AU
E3            3 --> GARRITY G/AU
E4            2     GARRITY G C/AU
E5           22     GARRITY G M/AU
E6            1     GARRITY GEORGE/AU
E7            6     GARRITY GEORGE M/AU
E8            1     GARRITY H M/AU
E9            3     GARRITY J/AU
E10          65     GARRITY J A/AU
E11           1     GARRITY J D/AU
E12           2     GARRITY J F/AU

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             2 "GARRITY G C"/AU
            22 "GARRITY G M"/AU
             1 "GARRITY GEORGE"/AU
             6 "GARRITY GEORGE M"/AU
L4          34 "GARRITY G"/AU OR "GARRITY G C"/AU OR "GARRITY G M"/AU OR "GARRI
               TY GEORGE"/AU OR "GARRITY GEORGE M"/AU

=> s l4 and names
          8496 NAMES
L5           0 L4 AND NAMES

=> s l4 and gene
        981774 GENE
        572427 GENES
       1163716 GENE
                 (GENE OR GENES)
L6           4 L4 AND GENE

=> d bib ab 1-4

L6   ANSWER 1 OF 4     MEDLINE on STN
Full Text
AN   2007472746     MEDLINE
DN   PubMed ID: 17586664
TI   Naive Bayesian classifier for rapid assignment of rRNA sequences into the
     new bacterial taxonomy.
AU   Wang Qiong; Garrity George M; Tiedje James M; Cole James R
CS   Center for Microbial Ecology, Michigan State University, East Lansing, MI
     48824, USA.
SO   Applied and environmental microbiology, (2007 Aug) Vol. 73, No. 16, pp.
     5261-7.  Electronic Publication: 2007-06-22.
     Journal code: 7605801. ISSN: 0099-2240.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
     (RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA   English
FS   Priority Journals
EM   200710
ED   Entered STN: 14 Aug 2007
     Last Updated on STN: 20 Oct 2007
     Entered Medline: 19 Oct 2007
AB   The Ribosomal Database Project (RDP) Classifier, a naive Bayesian
     classifier, can rapidly and accurately classify bacterial 16S rRNA
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sequences into the new higher-order taxonomy proposed in Bergey's Taxonomic Outline of the Prokaryotes (2nd ed., release 5.0, Springer-Verlag, New York, NY, 2004). It provides taxonomic assignments from domain to genus, with confidence estimates for each assignment. The majority of classifications (98%) were of high estimated confidence (> or = 95%) and high accuracy (98%). In addition to being tested with the corpus of 5,014 type strain sequences from Bergey's outline, the RDP Classifier was tested with a corpus of 23,095 rRNA sequences as assigned by the NCBI into their alternative higher-order taxonomy. The results from leave-one-out testing on both corpora show that the overall accuracies at all levels of confidence for near-full-length and 400-base segments were 89% or above down to the genus level, and the majority of the classification errors appear to be due to anomalies in the current taxonomies. For shorter rRNA segments, such as those that might be generated by pyrosequencing, the error rate varied greatly over the length of the 16S rRNA **gene,** with segments around the V2 and V4 variable regions giving the lowest error rates. The RDP Classifier is suitable both for the analysis of single rRNA sequences and for the analysis of libraries of thousands of sequences. Another related tool, RDP Library Compare, was developed to facilitate microbial-community comparison based on 16S rRNA **gene** sequence libraries. It combines the RDP Classifier with a statistical test to flag taxa differentially represented between samples. The RDP Classifier and RDP Library Compare are available online at http://rdp.cme.msu.edu/.

L6 ANSWER 2 OF 4 MEDLINE on STN
Full Text
AN 2005255708 MEDLINE
DN PubMed ID: 15731209
TI Self-organizing and self-correcting classifications of biological data.
AU **Garrity George M**; Lilburn Timothy G
CS Department of Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI 48824, USA.. garrityg@msu.edu
SO Bioinformatics (Oxford, England), (2005 May 15) Vol. 21, No. 10, pp. 2309-14. Electronic Publication: 2005-02-24.
Journal code: 9808944. ISSN: 1367-4803.
CY England: United Kingdom
DT (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
EM 200508
ED Entered STN: 18 May 2005
Last Updated on STN: 31 Aug 2005
Entered Medline: 30 Aug 2005
AB MOTIVATION: Rapid, automated means of organizing biological data are required if we hope to keep abreast of the flood of data emanating from sequencing, microarray and similar high-throughput analyses. Faced with the need to validate the annotation of thousands of sequences and to generate biologically meaningful classifications based on the sequence data, we turned to statistical methods in order to automate these processes. RESULTS: An algorithm for automated classification based on evolutionary distance data was written in S. The algorithm was tested on a dataset of 1436 small subunit ribosomal RNA sequences and was able to classify the sequences according to an extant scheme, use statistical measurements of group membership to detect sequences that were misclassified within this scheme and produce a new classification. In this study, the use of the algorithm to address problems in prokaryotic taxonomy is discussed. AVAILABILITY: S-Plus is available from Insightful, Inc. An S-Plus implementation of the algorithm and the associated data are available at http://taxoweb.rmmg.msu.edu/datasets

L6 ANSWER 3 OF 4 MEDLINE on STN
Full Text
AN 2004633031 MEDLINE
DN PubMed ID: 15608200
TI The Ribosomal Database Project (RDP-II): sequences and tools for high-throughput rRNA analysis.
AU Cole J R; Chai B; Farris R J; Wang Q; Kulam S A; McGarrell D M; **Garrity G M**; Tiedje J M
CS Center for Microbial Ecology, Michigan State University, East Lansing, MI

48824-4320, USA.. rdpstaff@msu.edu
SO Nucleic acids research, (2005 Jan 1) Vol. 33, No. Database issue, pp. D294-6.
Journal code: 0411011. E-ISSN: 1362-4962.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
EM 200504
ED Entered STN: 21 Dec 2004
Last Updated on STN: 17 Apr 2005
Entered Medline: 15 Apr 2005
AB The Ribosomal Database Project (RDP-II) provides the research community with aligned and annotated rRNA **gene** sequences, along with analysis services and a phylogenetically consistent taxonomic framework for these data. Updated monthly, these services are made available through the RDP-II website (http://rdp.cme.msu.edu/). RDP-II release 9.21 (August 2004) contains 101,632 bacterial small subunit rRNA **gene** sequences in aligned and annotated format. High-throughput tools for initial taxonomic placement, identification of related sequences, probe and primer testing, data navigation and subalignment download are provided. The RDP-II email address for questions or comments is rdpstaff@msu.edu.

L6 ANSWER 4 OF 4 MEDLINE on STN
Full Text
AN 93356958 MEDLINE
DN PubMed ID: 7688970
TI Genetic relationships among actinomycetes that produce the immunosuppressant macrolides FK506, FK520/FK523 and rapamycin.
AU **Garrity G M**; Heimbuch B K; Motamedi H; Shafiee A
CS Basic Microbiology Department, Merck Research Laboratories, Merck & Co., Rahway, NJ 07065.
SO Journal of industrial microbiology, (1993 Jan) Vol. 12, No. 1, pp. 42-7.
Journal code: 8610887. ISSN: 0169-4146.
CY ENGLAND: United Kingdom
DT (COMPARATIVE STUDY)
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Biotechnology
EM 199309
ED Entered STN: 9 Aug 1995
Last Updated on STN: 29 Jan 1999
Entered Medline: 22 Sep 1993
AB A polyphasic taxonomic study was undertaken to establish the genetic and phenotypic relationships among six actinomycetes that produce the immunosuppressant macrolides FK506, FK520/FK523 and rapamycin. Chemotaxonomic studies reveal that all have Type I cell walls. Gas chromatography (GC) of fatty acid methyl esters revealed patterns consistent for strains of Streptomyces with 16:0 and 15:0 anteiso predominating. Principal component analysis of GC data revealed distinct profiles for each culture. Reciprocal DNA homology studies at Tm-25 showed the rapamycin-producing strain and one FK506-producing strain to have 38-50% homology with the type strain of Streptomyces hygroscopicus (ATCC 27438). The remaining strains exhibited 6-17% homology. To further explore the relationships among these strains all were probed for the presence of an O-methyltransferase **gene** specific to this biosynthetic pathway. Among the strains of interest, only Streptomyces hygroscopicus subsp. yakushimaensis, the patent strain for FK520/FK523, failed to hybridize with the probes.

=> s l4 and (network or taxon? or resource or identifier)
92748 NETWORK
60941 NETWORKS
133375 NETWORK
(NETWORK OR NETWORKS)
20329 TAXON?
38778 RESOURCE
83791 RESOURCES
113633 RESOURCE
(RESOURCE OR RESOURCES)

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          988 IDENTIFIER
          844 IDENTIFIERS
         1744 IDENTIFIER
              (IDENTIFIER OR IDENTIFIERS)
L7         13 L4 AND (NETWORK OR TAXON? OR RESOURCE OR IDENTIFIER)

=> d bib ab 1-13

L7   ANSWER 1 OF 13     MEDLINE on STN
Full Text
AN   2008303121     MEDLINE
DN   PubMed ID: 18464787
TI   The minimum information about a genome sequence (MIGS) specification.
AU   Field Dawn; Garrity George; Gray Tanya; Morrison Norman; Selengut
     Jeremy; Sterk Peter; Tatusova Tatiana; Thomson Nicholas; Allen Michael J;
     Angiuoli Samuel V; Ashburner Michael; Axelrod Nelson; Baldauf Sandra;
     Ballard Stuart; Boore Jeffrey; Cochrane Guy; Cole James; Dawyndt Peter; De
     Vos Paul; DePamphilis Claude; Edwards Robert; Faruque Nadeem; Feldman
     Robert; Gilbert Jack; Gilna Paul; Glockner Frank Oliver; Goldstein Philip;
     Guralnick Robert; Haft Dan; Hancock David; Hermjakob Henning; Hertz-Fowler
     Christiane; Hugenholtz Phil; Joint Ian; Kagan Leonid; Kane Matthew;
     Kennedy Jessie; Kowalchuk George; Kottmann Renzo; Kolker Eugene; Kravitz
     Saul; Kyrpides Nikos; Leebens-Mack Jim; Lewis Suzanna E; Li Kelvin; Lister
     Allyson L; Lord Phillip; Maltsev Natalia; Markowitz Victor; Martiny
     Jennifer; Methe Barbara; Mizrachi Ilene; Moxon Richard; Nelson Karen;
     Parkhill Julian; Proctor Lita; White Owen; Sansone Susanna-Assunta; Spiers
     Andrew; Stevens Robert; Swift Paul; Taylor Chris; Tateno Yoshio; Tett
     Adrian; Turner Sarah; Ussery David; Vaughan Bob; Ward Naomi; Whetzel
     Trish; San Gil Ingio; Wilson Gareth; Wipat Anil
CS   Natural Environmental Research Council Centre for Ecology and Hydrology,
     Oxford OX1 3SR, UK.. dfield@ceh.ac.uk
NC   NIH0010074174
SO   Nature biotechnology, (2008 May) Vol. 26, No. 5, pp. 541-7.
     Journal code: 9604648. E-ISSN: 1546-1696.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
     (RESEARCH SUPPORT, NON-U.S. GOV'T)
LA   English
FS   Priority Journals
EM   200806
ED   Entered STN: 10 May 2008
     Last Updated on STN: 5 Jun 2008
     Entered Medline: 4 Jun 2008
AB   With the quantity of genomic data increasing at an exponential rate, it is
     imperative that these data be captured electronically, in a standard
     format.  Standardization activities must proceed within the auspices of
     open-access and international working bodies.  To tackle the issues
     surrounding the development of better descriptions of genomic
     investigations, we have formed the Genomic Standards Consortium (GSC).
     Here, we introduce the minimum information about a genome sequence (MIGS)
     specification with the intent of promoting participation in its
     development and discussing the resources that will be required to
     develop improved mechanisms of metadata capture and exchange.  As part of
     its wider goals, the GSC also supports improving the 'transparency' of the
     information contained in existing genomic databases.

L7   ANSWER 2 OF 13     MEDLINE on STN
Full Text
AN   2007472746     MEDLINE
DN   PubMed ID: 17586664
TI   Naive Bayesian classifier for rapid assignment of rRNA sequences into the
     new bacterial taxonomy.
AU   Wang Qiong; Garrity George M; Tiedje James M; Cole James R
CS   Center for Microbial Ecology, Michigan State University, East Lansing, MI
     48824, USA.
SO   Applied and environmental microbiology, (2007 Aug) Vol. 73, No. 16, pp.
     5261-7.  Electronic Publication: 2007-06-22.
     Journal code: 7605801. ISSN: 0099-2240.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
     (RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA   English
```

FS Priority Journals
EM 200710
ED Entered STN: 14 Aug 2007
Last Updated on STN: 20 Oct 2007
Entered Medline: 19 Oct 2007
AB The Ribosomal Database Project (RDP) Classifier, a naive Bayesian classifier, can rapidly and accurately classify bacterial 16S rRNA sequences into the new higher-order **taxonomy** proposed in Bergey's **Taxonomic** Outline of the Prokaryotes (2nd ed., release 5.0, Springer-Verlag, New York, NY, 2004). It provides **taxonomic** assignments from domain to genus, with confidence estimates for each assignment. The majority of classifications (98%) were of high estimated confidence (> or = 95%) and high accuracy (98%). In addition to being tested with the corpus of 5,014 type strain sequences from Bergey's outline, the RDP Classifier was tested with a corpus of 23,095 rRNA sequences as assigned by the NCBI into their alternative higher-order **taxonomy**. The results from leave-one-out testing on both corpora show that the overall accuracies at all levels of confidence for near-full-length and 400-base segments were 89% or above down to the genus level, and the majority of the classification errors appear to be due to anomalies in the current **taxonomies**. For shorter rRNA segments, such as those that might be generated by pyrosequencing, the error rate varied greatly over the length of the 16S rRNA gene, with segments around the V2 and V4 variable regions giving the lowest error rates. The RDP Classifier is suitable both for the analysis of single rRNA sequences and for the analysis of libraries of thousands of sequences. Another related tool, RDP Library Compare, was developed to facilitate microbial-community comparison based on 16S rRNA gene sequence libraries. It combines the RDP Classifier with a statistical test to flag taxa differentially represented between samples. The RDP Classifier and RDP Library Compare are available online at http://rdp.cme.msu.edu/.

L7 ANSWER 3 OF 13 MEDLINE on STN
Full Text
AN 2006490108 MEDLINE
DN PubMed ID: 16772262
TI Computational aspects of systematic biology.
AU Lilburn Timothy G; Harrison Scott H; Cole James R; **Garrity George M**
CS Department of Microbiology and Molecular Genetics at Michigan State University, East Lansing MI, USA.
SO Briefings in bioinformatics, (2006 Jun) Vol. 7, No. 2, pp. 186-95. Electronic Publication: 2006-04-24. Ref: 60
Journal code: 100912837. ISSN: 1467-5463.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
General Review; (REVIEW)
LA English
FS Priority Journals
EM 200609
ED Entered STN: 19 Aug 2006
Last Updated on STN: 13 Sep 2006
Entered Medline: 12 Sep 2006
AB We review the **resources** available to systematic biologists who wish to use computers to build classifications. Algorithm development is in an early stage, and only a few examples of integrated applications for systematic biology are available. The availability of data is crucial if systematic biology is to enter the computer age.

L7 ANSWER 4 OF 13 MEDLINE on STN
Full Text
AN 2005255708 MEDLINE
DN PubMed ID: 15731209
TI Self-organizing and self-correcting classifications of biological data.
AU **Garrity George M**; Lilburn Timothy G
CS Department of Microbiology and Molecular Genetics, Michigan State University, East Lansing, MI 48824, USA.. garrity@msu.edu
SO Bioinformatics (Oxford, England), (2005 May 15) Vol. 21, No. 10, pp. 2309-14. Electronic Publication: 2005-02-24.
Journal code: 9808944. ISSN: 1367-4803.
CY England: United Kingdom

DT (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
EM 200508
ED Entered STN: 18 May 2005
Last Updated on STN: 31 Aug 2005
Entered Medline: 30 Aug 2005
AB MOTIVATION: Rapid, automated means of organizing biological data are required if we hope to keep abreast of the flood of data emanating from sequencing, microarray and similar high-throughput analyses. Faced with the need to validate the annotation of thousands of sequences and to generate biologically meaningful classifications based on the sequence data, we turned to statistical methods in order to automate these processes. RESULTS: An algorithm for automated classification based on evolutionary distance data was written in S. The algorithm was tested on a dataset of 1436 small subunit ribosomal RNA sequences and was able to classify the sequences according to an extant scheme, use statistical measurements of group membership to detect sequences that were misclassified within this scheme and produce a new classification. In this study, the use of the algorithm to address problems in prokaryotic **taxonomy** is discussed. AVAILABILITY: S-Plus is available from Insightful, Inc. An S-Plus implementation of the algorithm and the associated data are available at http://taxoweb.mmg.msu.edu/datasets

L7 ANSWER 5 OF 13 MEDLINE on STN
Full Text
AN 2005026616 MEDLINE
DN PubMed ID: 15653930
TI Nomenclature and **taxonomy** of the genus Salmonella.
AU Tindall B J; Grimont P A D; **Garrity G M**; Euzeby J P
CS DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Mascheroder Weg 1b, D-38124 Braunschweig, Germany.. bti@dsmz.de
SO International journal of systematic and evolutionary microbiology, (2005 Jan) Vol. 55, No. Pt 1, pp. 521-4.
Journal code: 100899600. ISSN: 1466-5026.
CY England: United Kingdom
DT Commentary
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200503
ED Entered STN: 19 Jan 2005
Last Updated on STN: 4 Mar 2005
Entered Medline: 3 Mar 2005
AB The nomenclature of the genus Salmonella has reached an unsatisfactory state of affairs, with two systems of nomenclature in circulation. One system, proposed in the 1980s by Le Minor and Popoff, has received wide acceptance, although it does not conform to the rules of the Bacteriological Code. The other system, which conforms to the rules of the Bacteriological Code, is being used by an ever-decreasing minority. As a result of a number of recent Requests for an Opinion, the Judicial Commission of the International Committee on the Systematics of Prokaryotes has issued an Opinion (Opinion 80) with the intention that it should solve these discrepancies. However, like all Opinions, it is limited to matters of nomenclature and does not help to interpret the **taxonomic** consequences. The Judicial Commission has therefore asked experts in the field of nomenclature and **taxonomy** to write a commentary on the nomenclatural and **taxonomic** consequences of Opinion 80. The present article explains the nomenclatural consequences of Opinion 80, together with a clear presentation of the **taxonomy** that results when applying the currently widely accepted interpretation that the genus Salmonella currently includes only two species.

L7 ANSWER 6 OF 13 MEDLINE on STN
Full Text
AN 2004633031 MEDLINE
DN PubMed ID: 15608200
TI The Ribosomal Database Project (RDP-II): sequences and tools for high-throughput rRNA analysis.
AU Cole J R; Chai B; Farris R J; Wang Q; Kulam S A; McGarrell D M; **Garrity G**

M; Tiedje J M
CS Center for Microbial Ecology, Michigan State University, East Lansing, MI 48824-4320, USA.. rdpstaff@msu.edu
SO Nucleic acids research, (2005 Jan 1) Vol. 33, No. Database issue, pp. D294-6.
Journal code: 0411011. E-ISSN: 1362-4962.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
EM 200504
ED Entered STN: 21 Dec 2004
Last Updated on STN: 17 Apr 2005
Entered Medline: 15 Apr 2005
AB The Ribosomal Database Project (RDP-II) provides the research community with aligned and annotated rRNA gene sequences, along with analysis services and a phylogenetically consistent **taxonomic** framework for these data. Updated monthly, these services are made available through the RDP-II website (http://rdp.cme.msu.edu/). RDP-II release 9.21 (August 2004) contains 101,632 bacterial small subunit rRNA gene sequences in aligned and annotated format. High-throughput tools for initial **taxonomic** placement, identification of related sequences, probe and primer testing, data navigation and subalignment download are provided. The RDP-II email address for questions or comments is rdpstaff@msu.edu.

L7 ANSWER 7 OF 13 MEDLINE on STN
Full Text
AN 2004041650 MEDLINE
DN PubMed ID: 14742453
TI Exploring prokaryotic **taxonomy**.
AU Lilburn Timothy G; **Garrity George M**
CS Bioinformatics Group, American Type Culture Collection, Manassas, VA 20110, USA.
SO International journal of systematic and evolutionary microbiology, (2004 Jan) Vol. 54, No. Pt 1, pp. 7-13.
Journal code: 100899600. ISSN: 1466-5026.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
EM 200403
ED Entered STN: 27 Jan 2004
Last Updated on STN: 30 Mar 2004
Entered Medline: 29 Mar 2004
AB Techniques drawn from exploratory data analysis, using tools found in the S-Plus statistical software package, have been used to inspect and maintain the Bergey's **Taxonomic** Outline and to move towards an automated and community-based means of working on the outline. These techniques can be used to classify sequences from unnamed and uncultured organisms, to visualize errors in the **taxonomy** or in the curation of the sequences, to suggest emendations to the **taxonomy** or to the classification of extant species and to complement the visualization of phylogenies based on treeing methods. A dataset of more than 9200 aligned small-subunit rRNA sequences was analysed in the context of the current **taxonomic** outline. The use of the algorithm in exploring and modifying the **taxonomy** is illustrated with an example drawn from the family Comamonadaceae.

L7 ANSWER 8 OF 13 MEDLINE on STN
Full Text
AN 2003023388 MEDLINE
DN PubMed ID: 12520046
TI The Ribosomal Database Project (RDP-II): previewing a new autoaligner that allows regular updates and the new prokaryotic **taxonomy**.
AU Cole J R; Chai B; Marsh T L; Farris R J; Wang Q; Kulam S A; Chandra S; McGarrell D M; Schmidt T M; **Garrity G M**; Tiedje J M
CS Center for Microbial Ecology, 2225A Biomedical Physical Sciences, Michigan State University, East Lansing, MI 48824-4320, USA. (Ribosomal Database Project). rdpstaff@msu.edu
SO Nucleic acids research, (2003 Jan 1) Vol. 31, No. 1, pp. 442-3.
Journal code: 0411011. E-ISSN: 1362-4962.

CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
EM 200303
ED Entered STN: 18 Jan 2003
Last Updated on STN: 16 Mar 2003
Entered Medline: 14 Mar 2003
AB The Ribosomal Database Project-II (RDP-II) pro-vides data, tools and services related to ribosomal RNA sequences to the research community. Through its website (http://rdp.cme.msu.edu), RDP-II offers aligned and annotated rRNA sequence data, analysis services, and phylogenetic inferences (trees) derived from these data. RDP-II release 8.1 contains 16 277 prokaryotic, 5201 eukaryotic, and 1503 mitochondrial small subunit rRNA sequences in aligned and annotated format. The current public beta release of 9.0 debuts a new regularly updated alignment of over 50 000 annotated (eu)bacterial sequences. New analysis services include a sequence search and selection tool (Hierarchy Browser) and a phylogenetic tree building and visualization tool (Phylip Interface). A new interactive tutorial guides users through the basics of rRNA sequence analysis. Other services include probe checking, phylogenetic placement of user sequences, screening of users' sequences for chimeric rRNA sequences, automated alignment, production of similarity matrices, and services to plan and analyze terminal restriction fragment polymorphism (T-RFLP) experiments. The RDP-II email address for questions or comments is rdpstaff@msu.edu.

L7 ANSWER 9 OF 13 MEDLINE on STN
Full Text
AN 2001106573 MEDLINE
DN PubMed ID: 11125082
TI The RDP-II (Ribosomal Database Project).
AU Maidak B L; Cole J R; Lilburn T G; Parker C T Jr; Saxman P R; Farris R J; **Garrity G M**; Olsen G J; Schmidt T M; Tiedje J M
CS Center for Microbial Ecology, 540 Plant and Soil Sciences Building, Michigan State University, East Lansing, MI 48824-1325, USA.
SO Nucleic acids research, (2001 Jan 1) Vol. 29, No. 1, pp. 173-4.
Journal code: 0411011. E-ISSN: 1362-4962.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
EM 200102
ED Entered STN: 22 Mar 2001
Last Updated on STN: 21 May 2001
Entered Medline: 8 Feb 2001
AB The Ribosomal Database Project (RDP-II), previously described by Maidak et al. [Nucleic Acids Res. (2000), 28, 173-174], continued during the past year to add new rRNA sequences to the aligned data and to improve the analysis commands. Release 8.0 (June 1, 2000) consisted of 16 277 aligned prokaryotic small subunit (SSU) rRNA sequences while the number of eukaryotic and mitochondrial SSU rRNA sequences in aligned form remained at 2055 and 1503, respectively. The number of prokaryotic SSU rRNA sequences more than doubled from the previous release 14 months earlier, and approximately 75% are longer than 899 bp. An RDP-II mirror site in Japan is now available (http://wdcm.nig.ac.jp/RDP/html/index.h tml). RDP-II provides aligned and annotated rRNA sequences, derived phylogenetic trees and **taxonomic** hierarchies, and analysis services through its WWW server (http://rdp.cme.msu.edu/). Analysis services include rRNA probe checking, approximate phylogenetic placement of user sequences, screening user sequences for possible chimeric rRNA sequences, automated alignment, production of similarity matrices and services to plan and analyze terminal restriction fragment polymorphism experiments. The RDP-II email address for questions and comments has been changed from curator@cme.msu.edu to rdpstaff@msu.edu.

L7 ANSWER 10 OF 13 MEDLINE on STN
Full Text

AN 2000063250 MEDLINE
DN PubMed ID: 10592216
TI The RDP (Ribosomal Database Project) continues.
AU Maidak B L; Cole J R; Lilburn T G; Parker C T Jr; Saxman P R; Stredwick J M; **Garrity G M**; Li B; Olsen G J; Pramanik S; Schmidt T M; Tiedje J M
CS Center for Microbial Ecology, 540 Plant and Soil Sciences Building, Michigan State University, East Lansing, MI 48824-1325, USA.. curator@cme.msu.edu
SO Nucleic acids research, (2000 Jan 1) Vol. 28, No. 1, pp. 173-4. Journal code: 0411011. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
(RESEARCH SUPPORT, NON-U.S. GOV'T)
(RESEARCH SUPPORT, U.S. GOV'T, NON-P.H.S.)
LA English
FS Priority Journals
EM 200002
ED Entered STN: 14 Mar 2000
Last Updated on STN: 14 Mar 2000
Entered Medline: 25 Feb 2000
AB The Ribosomal Database Project (RDP-II), previously described by Maidak et al., continued during the past year to add new rRNA sequences to the aligned data and to improve the analysis commands. Release 7.1 (September 17, 1999) included more than 10 700 small subunit rRNA sequences. More than 850 type strain sequences were identified and added to the prokaryotic alignment, bringing the total number of type sequences to 3324 representing 2460 different species. Availability of an RDP-II mirror site in Japan is also near completion. RDP-II provides aligned and annotated rRNA sequences, derived phylogenetic trees and **taxonomic** hierarchies, and analysis services through its WWW server (http://rdp.cme.msu.edu/). Analysis services include rRNA probe checking, approx-i-mate phylogenetic placement of user sequences, screening user sequences for possible chimeric rRNA sequences, automated alignment, production of similarity matrices and services to plan and analyze terminal restriction fragment length polymorphism (T-RFLP) experiments.

L7 ANSWER 11 OF 13 MEDLINE on STN
Full Text
AN 1999316456 MEDLINE
DN PubMed ID: 10383870
TI Bioprospecting in the developing world.
AU **Garrity G M**; Hunter-Cevera J
CS Department of Microbiology, Bergey's Manual Trust, 152 Giltner Hall, Michigan State University, East Lansing, MI 48824-1101, USA.. wgarrity@pilot.msu.edu
SO Current opinion in microbiology, (1999 Jun) Vol. 2, No. 3, pp. 236-40. Ref: 34
Journal code: 9815056. ISSN: 1369-5274.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
LA English
FS Priority Journals
EM 199907
ED Entered STN: 30 Jul 1999
Last Updated on STN: 30 Jul 1999
Entered Medline: 21 Jul 1999
AB During the past ten years, species-rich nations in the developing world have sought to capitalize on their 'biological patrimony' through a variety of business relationships with multinational corporations as a means of underwriting their conservation efforts. Initially lauded, these relationships have generated more rhetoric than revenues to date. The ramifications of these results on bioprospecting are discussed along with the foreseeable changes in models of collaboration.

L7 ANSWER 12 OF 13 MEDLINE on STN
Full Text
AN 93356958 MEDLINE
DN PubMed ID: 7688970
TI Genetic relationships among actinomycetes that produce the immunosuppressant macrolides FK506, FK520/FK523 and rapamycin.

AU **Garrity G M**; Heimbuch B K; Motamedi H; Shafiee A
CS Basic Microbiology Department, Merck Research Laboratories, Merck & Co., Rahway, NJ 07065.
SO Journal of industrial microbiology, (1993 Jan) Vol. 12, No. 1, pp. 42-7. Journal code: 8610887. ISSN: 0169-4146.
CY ENGLAND: United Kingdom
DT (COMPARATIVE STUDY)
    Journal; Article; (JOURNAL ARTICLE)
LA English
FS Biotechnology
EM 199309
ED Entered STN: 9 Aug 1995
    Last Updated on STN: 29 Jan 1999
    Entered Medline: 22 Sep 1993
AB A polyphasic **taxonomic** study was undertaken to establish the genetic and phenotypic relationships among six actinomycetes that produce the immunosuppressant macrolides FK506, FK520/FK523 and rapamycin. Chemotaxonomic studies reveal that all have Type I cell walls. Gas chromatography (GC) of fatty acid methyl esters revealed patterns consistent for strains of Streptomyces with 16:0 and 15:0 anteiso predominating. Principal component analysis of GC data revealed distinct profiles for each culture. Reciprocal DNA homology studies at Tm-25 showed the rapamycin-producing strain and one FK506-producing strain to have 38-50% homology with the type strain of Streptomyces hygroscopicus (ATCC 27438). The remaining strains exhibited 6-17% homology. To further explore the relationships among these strains all were probed for the presence of an O-methyltransferase gene specific to this biosynthetic pathway. Among the strains of interest, only Streptomyces hygroscopicus subsp. yakushimaensis, the patent strain for FK520/FK523, failed to hybridize with the probes.

L7 ANSWER 13 OF 13 MEDLINE on STN
Full Text
AN 91302170 MEDLINE
DN PubMed ID: 1906451
TI Novel and potent gastrin and brain cholecystokinin antagonists from Streptomyces olivaceus. **Taxonomy**, fermentation, isolation, chemical conversions, and physico-chemical and biochemical properties.
AU Lam Y K; Bogen D; Chang R S; Faust K A; Hensens O D; Zink D L; Schwartz C D; Zitano L; **Garrity G M**; Gagliardi M M; +
CS Merck Sharp & Dohme Research Laboratories, Rahway, New Jersey 07065.
SO The Journal of antibiotics, (1991 Jun) Vol. 44, No. 6, pp. 613-25. Journal code: 0151115. ISSN: 0021-8820.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199108
ED Entered STN: 8 Sep 1991
    Last Updated on STN: 8 Sep 1991
    Entered Medline: 21 Aug 1991
AB The discovery and physico-chemical characterization of three novel and minor virginiamycin M1 analogs as potent gastrin antagonists from a culture of a strain of Streptomyces olivaceus are described. These analogs are L-156,586, L-156,587 and L-156,588. They are, respectively, 15-dihydro-13,14-anhydro-, 13,14-anhydro- and 13-desoxy-analogs of virginiamycin M1. We also chemically converted virginiamycin M1 (via L-156,587) to L-156,586 and its unnatural epimer, L-156,906. These analogs are competitive and selective antagonists of gastrin and brain cholecystokinin binding at nanomolar concentrations. These are the most potent gastrin/brain cholecystokinin antagonists from natural products. The same compounds showed poor Gram-positive antibiotic activity versus virginiamycin M1. Structurally related Gram-positive antibiotics, griseoviridin and madumycin I, were inactive in gastrin and brain cholecystokinin binding at up to 100 microM.

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    (FILE 'HOME' ENTERED AT 09:39:40 ON 11 JUN 2008)

    INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,

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     AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
     CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
     DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 09:40:08 ON 11 JUN 2008
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               331   FILE USPAT2
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     FILE 'MEDLINE, CAPLUS, SCISEARCH, EMBASE' ENTERED AT 09:43:33 ON 11 JUN
     2008
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L3            10 DUP REM L2 (9 DUPLICATES REMOVED)

     FILE 'MEDLINE' ENTERED AT 09:45:00 ON 11 JUN 2008
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L4            34 S E3 OR E4 OR E5 OR E6 OR E7
L5             0 S L4 AND NAMES
L6             4 S L4 AND GENE
L7            13 S L4 AND (NETWORK OR TAXON? OR RESOURCE OR IDENTIFIER)


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